

AMENDMENTS TO THE SPECIFICATION

Please amend page 3, line 25 through page 4, line 14, as follows:

Figure 2 depicts a partial labeling of adenosine in a DNA subsample in accordance with one embodiment of the disclosed methods and devices and an exemplary method for constructing a nucleotide time map 310, 320, 330, 340 (as shown in Figure 3) for one type of labeled nucleotide 220, based on measured times between labeled nucleotides 220 in a number of complementary nucleic acid strands 230, 240, 250. The times between labeled nucleotides 220 may be compiled into a time map 310, 320, 330, 340 (as shown in Figure 3) for each type of nucleotides labeled as described herein. Distances between the labelled nucleotides 220 may then be calculated from these time maps 310, 320, 330, 340 (as shown in Figure 3). The sequence 210 of the complementary strand 230, 240, 250 is shown, along with exemplary locations for labeled nucleotides 220. As indicated 260, where identical nucleotides are located adjacent to each other, this will be detected as an increased frequency of labeling at that location;

Figure 3 depicts how a complementary DNA sequence 210 may be assembled by aligning the four nucleotide time separation maps 310, 320, 330, 340 according to the non-overlapping rules. The template nucleic acid 200 will be an exact complement of the determined sequence 210. Computerized and statistical tools can assist in this process.

Figure 4 depicts an exemplary method for constructing 450 time maps 310, 320, 330, 340 (as shown in Figure 3) for labeled nucleotides 220.

Figure 5 illustrates an exemplary method for aligning 520 time maps 310, 320, 330, 340 (as shown in Figure 3) to obtain a nucleic acid sequence 200 of the complementary strand 210.